WHAT IS CLAIMED IS:

1. A method for producing a preponderance of gas phase ions having higher order charge states during laser desorption ionization of an analyte, the method comprising:

irradiating the analyte in the presence of energy absorbing molecules at a mid-IR wavelength that is offset from an IR absorption maximum of the energy absorbing molecules.

2. The method of claim 1, wherein the analyte is within a matrix of said energy absorbing molecules.

3. The method of claim 1, wherein the energy absorbing molecules are photoactive components of a SEND surface upon which the analyte is disposed.

4. The method of claim 1, wherein said mid-IR wavelength is produced by a fixed wavelength laser.

5. The method of claim 1, wherein said mid-IR wavelength is produced by a tunable laser.

6. The method of claim 5, wherein the laser is a tunable optical parametric oscillator (OPO) infrared laser.

7. The method of claim 1, further comprising the subsequent step of:

detecting at least a plurality of said higher order charge state gas phase ions.

8. The method of claim 7, wherein said detecting is performed using a device selected from the group consisting of: ion mobility spectrometer, total ion current measuring device, and mass spectrometer.

9. The method of claim 8, wherein said detecting is performed using a mass spectrometer.

10. The method of claim 9, wherein said detecting further includes a mass spectral analysis.

11. The method of claim 10, wherein said mass spectrometer is a tandem mass spectrometer and said mass spectral analysis is a tandem mass spectral analysis.

12. The method of claim 11, wherein said tandem mass spectrometer is selected from the group consisting of QqTOF mass spectrometer, triple quadrupole mass spectrometer, ion trap mass spectrometer, ion trap time-of-flight (TOF) mass spectrometer, ion cyclotron resonance (ICR) mass spectrometer, time-of-flight time-of-flight (TOF-TOF) mass spectrometer, Fourier transform ion cyclotron resonance mass spectrometer, electric sector-magnetic sector mass spectrometer, magnetic sector-electric sector mass spectrometer, and electric sector-electric sector mass spectrometer.

13. The method of claim 12, wherein said tandem mass spectrometer is a QqTOF MS.

14. The method of claim 11, wherein said tandem mass spectral analysis comprises:

selecting at least a first ion species;

fragmenting said at least first ion species into a plurality of product ion species; and then

performing a mass spectral analysis on at least one of said product ion species.

15. The method of claim 14, wherein said selected first ion species has a mass greater than about 5000 daltons.

16. The method of claim 15, wherein said selected first ion species has a mass greater than about 10,000 daltons.

17. The method of claim 16, wherein said selected first ion species has a mass greater than about 15,000 daltons.

18. The method of claim 17, wherein said selected first ion species has a mass greater than about 25,000 daltons.

19. The method of claim 14, wherein said fragmenting is performed by collision induced dissociation.

20. The method of claim 14, wherein said mass spectral analysis comprises a product ion scan of said product ions.

21. The method of claim 1, further comprising the antecedent step of:

adsorbing said analyte from an inhomogeneous sample directly onto a SELDI probe.

22. The method of claim 21, wherein said SELDI probe is a SEND probe.

23. The method of claim 21, further comprising the step, after adsorbing and before irradiating the analyte, of:

contacting said probe-adsorbed analyte with energy absorbing molecules.

24. The method of claim 1, wherein said analyte is a protein.

25. The method of 24, further comprising a later step of:

determining at least a partial amino acid sequence of said protein analyte.

26. The method of claim 25, wherein said partial amino acid sequence is determined at least in part by calculating differences in masses among product ions represented in a product ion scan.

27. The method of claim 26, further comprising a later step of identifying said protein analyte by querying a database with at least a portion of said at least partial protein sequence.

28. The method of claim 24, further comprising a later step of identifying said protein, wherein said identifying comprises:

comparing a product ion scan of said protein analyte to product ion scans predicted from protein or nucleic acid sequence databases; and then

using the most similar predicted product ion scan to identify said protein analyte.